

# Jerry StÅ¥hlberg

## List of Publications by Year in descending order

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81  
papers

7,160  
citations

61984

43  
h-index

64796

79  
g-index

82  
all docs

82  
docs citations

82  
times ranked

5127  
citing authors

#	ARTICLE	IF	CITATIONS
1	Glucomannan and beta-glucan degradation by <i>Mytilus edulis</i> Cel45A: Crystal structure and activity comparison with GH45 subfamily A, B and C. <i>Carbohydrate Polymers</i> , 2022, 277, 118771.	10.2	3
2	Machine learning reveals sequence-function relationships in family 7 glycoside hydrolases. <i>Journal of Biological Chemistry</i> , 2021, 297, 100931.	3.4	13
3	Reply to Cosgrove: Non-enzymatic action of expansins. <i>Journal of Biological Chemistry</i> , 2020, 295, 6783.	3.4	0
4	Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. <i>Molecular Cell</i> , 2020, 77, 927-929.	9.7	71
5	The hydrolysis mechanism of a GH45 cellulase and its potential relation to lytic transglycosylase and expansin function. <i>Journal of Biological Chemistry</i> , 2020, 295, 4477-4487.	3.4	16
6	Antibacterial pyrrolidinyl and piperidinyl substituted 2,4-diacetylphloroglucinols from <i>Pseudomonas protegens</i> UP46. <i>Journal of Antibiotics</i> , 2020, 73, 739-747.	2.0	3
7	The dissociation mechanism of processive cellulases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23061-23067.	7.1	40
8	Advantages of a distant cellulase catalytic base. <i>Journal of Biological Chemistry</i> , 2018, 293, 4680-4687.	3.4	5
9	Enantioselective Binding of Propranolol and Analogues Thereof to Cellobiohydrolase Cel7A. <i>Chemistry - A European Journal</i> , 2018, 24, 17975-17985.	3.3	5
10	Side-by-side biochemical comparison of two lytic polysaccharide monooxygenases from the white-rot fungus <i>Heterobasidion irregulare</i> on their activity against crystalline cellulose and glucomannan. <i>PLoS ONE</i> , 2018, 13, e0203430.	2.5	7
11	Correlation of structure, function and protein dynamics in GH7 cellobiohydrolases from <i>Trichoderma atroviride</i> , <i>T. reesei</i> and <i>T. harzianum</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 5.	6.2	37
12	Development of minimal enzyme cocktails for hydrolysis of sulfite-pulped lignocellulosic biomass. <i>Journal of Biotechnology</i> , 2017, 246, 16-23.	3.8	59
13	Improving the thermal stability of cellobiohydrolase Cel7A from <i>Hypocrea jecorina</i> by directed evolution. <i>Journal of Biological Chemistry</i> , 2017, 292, 17418-17430.	3.4	52
14	Biochemical and Structural Characterizations of Two <i>Dictyostelium</i> Cellobiohydrolases from the Amoebozoa Kingdom Reveal a High Level of Conservation between Distant Phylogenetic Trees of Life. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3395-3409.	3.1	13
15	Who's on base? Revealing the catalytic mechanism of inverting family 6 glycoside hydrolases. <i>Chemical Science</i> , 2016, 7, 5955-5968.	7.4	27
16	Sequencing, biochemical characterization, crystal structure and molecular dynamics of cellobiohydrolase Cel7A from <i>Geotrichum candidum</i> 3C. <i>FEBS Journal</i> , 2015, 282, 4515-4537.	4.7	37
17	Structural insights into the inhibition of cellobiohydrolase Cel7A by xylooligosaccharides. <i>FEBS Journal</i> , 2015, 282, 2167-2177.	4.7	25
18	Fungal Cellulases. <i>Chemical Reviews</i> , 2015, 115, 1308-1448.	47.7	673

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19	Quantum mechanical calculations suggest that lytic polysaccharide monooxygenases use a copper-oxy, oxygen-rebound mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 149-154.	7.1	210
20	Adaptation of <i>Dekkera bruxellensis</i> to lignocellulose-based substrate. Biotechnology and Applied Biochemistry, 2014, 61, 51-57.	3.1	17
21	Expression, crystal structure and cellulase activity of the thermostable cellobiohydrolase Cel7A from the fungus <i>Humicola grisea</i> var. <i>thermoidea</i> . Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2356-2366.	2.5	26
22	Towards a molecular-level theory of carbohydrate processivity in glycoside hydrolases. Current Opinion in Biotechnology, 2014, 27, 96-106.	6.6	89
23	The Mechanism of Cellulose Hydrolysis by a Two-Step, Retaining Cellobiohydrolase Elucidated by Structural and Transition Path Sampling Studies. Journal of the American Chemical Society, 2014, 136, 321-329.	13.7	164
24	Structural and Electronic Snapshots during the Transition from a Cu(II) to Cu(I) Metal Center of a Lytic Polysaccharide Monooxygenase by X-ray Photoreduction. Journal of Biological Chemistry, 2014, 289, 18782-18792.	3.4	99
25	Carbohydrate-Protein Interactions That Drive Processive Polysaccharide Translocation in Enzymes Revealed from a Computational Study of Cellobiohydrolase Processivity. Journal of the American Chemical Society, 2014, 136, 8810-8819.	13.7	95
26	Crystal Structure and Computational Characterization of the Lytic Polysaccharide Monooxygenase GH61D from the Basidiomycota Fungus <i>Phanerochaete chrysosporium</i> . Journal of Biological Chemistry, 2013, 288, 12828-12839.	3.4	158
27	The Structure of a Bacterial Cellobiohydrolase: The Catalytic Core of the Thermobifida fusca Family GH6 Cellobiohydrolase Cel6B. Journal of Molecular Biology, 2013, 425, 622-635.	4.2	34
28	Rational design, synthesis, evaluation and enzyme-substrate structures of improved fluorogenic substrates for family 6 glycoside hydrolases. FEBS Journal, 2013, 280, 184-198.	4.7	14
29	Enhanced ethanol production from wheat straw by integrated storage and pre-treatment (ISP). Enzyme and Microbial Technology, 2013, 52, 105-110.	3.2	26
30	Structural, Biochemical, and Computational Characterization of the Glycoside Hydrolase Family 7 Cellobiohydrolase of the Tree-killing Fungus <i>Heterobasidion irregulare</i> . Journal of Biological Chemistry, 2013, 288, 5861-5872.	3.4	70
31	Loop Motions Important to Product Expulsion in the Thermobifida fusca Glycoside Hydrolase Family 6 Cellobiohydrolase from Structural and Computational Studies. Journal of Biological Chemistry, 2013, 288, 33107-33117.	3.4	31
32	Glycosylated linkers in multimodular lignocellulose-degrading enzymes dynamically bind to cellulose. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14646-14651.	7.1	149
33	Product Binding Varies Dramatically between Processive and Nonprocessive Cellulase Enzymes. Journal of Biological Chemistry, 2012, 287, 24807-24813.	3.4	57
34	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.	7.3	210
35	The Putative Endoglucanase PcGH61D from <i>Phanerochaete chrysosporium</i> Is a Metal-Dependent Oxidative Enzyme that Cleaves Cellulose. PLoS ONE, 2011, 6, e27807.	2.5	226
36	Fermentation of lignocellulosic hydrolysate by the alternative industrial ethanol yeast <i>Dekkera bruxellensis</i> . Letters in Applied Microbiology, 2011, 53, 73-78.	2.2	34

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37	Improved bio-energy yields via sequential ethanol fermentation and biogas digestion of steam exploded oat straw. <i>Bioresource Technology</i> , 2011, 102, 4449-4455.	9.6	112
38	Hypocrea jecorina CEL6A protein engineering. <i>Biotechnology for Biofuels</i> , 2010, 3, 20.	6.2	55
39	Synthesis of Cyclic Î²-Glucan Using Laminarinase 16A Glycosynthase Mutant from the Basidiomycete <i>Phanerochaete chrysosporium</i> . <i>Journal of the American Chemical Society</i> , 2010, 132, 1724-1730.	13.7	22
40	Airtight storage of moist wheat grain improves bioethanol yields. <i>Biotechnology for Biofuels</i> , 2009, 2, 16.	6.2	17
41	X-ray crystal structures of <i>Phanerochaete chrysosporium</i> Laminarinase 16A in complex with products from lichenin and laminarin hydrolysis. <i>FEBS Journal</i> , 2009, 276, 3858-3869.	4.7	30
42	Three-dimensional Crystal Structure and Enzymic Characterization of Î²-Mannanase Man5A from Blue Mussel <i>Mytilus edulis</i> . <i>Journal of Molecular Biology</i> , 2006, 357, 1500-1510.	4.2	76
43	X-ray crystallographic native sulfur SAD structure determination of laminarinase Lam16A from <i>Phanerochaete chrysosporium</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1422-1429.	2.5	13
44	Structures of <i>Phanerochaete chrysosporium</i> Cel7D in complex with product and inhibitors. <i>FEBS Journal</i> , 2005, 272, 1952-1964.	4.7	44
45	Structural and biochemical studies of GH family 12 cellulases: improved thermal stability, and ligand complexes. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 246-291.	2.9	113
46	Crystal Complex Structures Reveal How Substrate is Bound in the â´4 to the +2 Binding Sites of <i>Humicola grisea</i> Cel12A. <i>Journal of Molecular Biology</i> , 2004, 342, 1505-1517.	4.2	32
47	Structure-Reactivity Studies of <i>Trichoderma reesei</i> Cellobiohydrolase Cel7A. <i>ACS Symposium Series</i> , 2004, , 207-226.	0.5	4
48	Dextranase from <i>Penicillium minioluteum</i> . <i>Structure</i> , 2003, 11, 1111-1121.	3.3	80
49	The catalytic module of Cel7D from <i>Phanerochaete chrysosporium</i> as a chiral selector: structural studies of its complex with the beta blocker (R)-propranolol. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 637-643.	2.5	11
50	Engineering the Exo-loop of <i>Trichoderma reesei</i> Cellobiohydrolase, Cel7A. A comparison with <i>Phanerochaete chrysosporium</i> Cel7D. <i>Journal of Molecular Biology</i> , 2003, 333, 817-829.	4.2	152
51	The Active Site of Cellobiohydrolase Cel6A from <i>Trichoderma reesei</i> : The Roles of Aspartic Acids D221 and D175. <i>Journal of the American Chemical Society</i> , 2002, 124, 10015-10024.	13.7	133
52	Preparation and crystallization of selenomethionyl dextranase from <i>Penicillium minioluteum</i> expressed in <i>Pichia pastoris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 346-348.	2.5	23
53	Crystallization and X-ray analysis of native and selenomethionyl Î²-mannanase Man5A from blue mussel, <i>Mytilus edulis</i> , expressed in <i>Pichia pastoris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 542-545.	2.5	10
54	Structural basis for enantiomer binding and separation of a common Î²-blocker: crystal structure of cellobiohydrolase Cel7A with bound (S)-propranolol at 1.9 Å... resolution. <i>Journal of Molecular Biology</i> , 2001, 305, 79-93.	4.2	61

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55	Family 7 cellobiohydrolases from <i>Phanerochaete chrysosporium</i> : crystal structure of the catalytic module of Cel7D (CBH58) at 1.32 Å... resolution and homology models of the isozymes. <i>Journal of Molecular Biology</i> , 2001, 314, 1097-1111.	4.2	101
56	The X-ray crystal structure of the <i>Trichoderma reesei</i> family 12 endoglucanase 3, Cel12A, at 1.9 Å... resolution1 1Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 2001, 308, 295-310.	4.2	121
57	Characterization of protein glycoforms with N-linked neutral and phosphorylated oligosaccharides: studies on the glycosylation of endoglucanase 1 (Cel7B) from <i>Trichoderma reesei</i> . <i>Biotechnology and Applied Biochemistry</i> , 2001, 33, 141.	3.1	32
58	Engineering of a glycosidase Family 7 cellobiohydrolase to more alkaline pH optimum: the pH behaviour of <i>Trichoderma reesei</i> Cel7A and its E223S/ A224H/L225V/T226A/D262G mutant. <i>Biochemical Journal</i> , 2001, 356, 19-30.	3.7	59
59	Engineering of a glycosidase Family 7 cellobiohydrolase to more alkaline pH optimum: the pH behaviour of <i>Trichoderma reesei</i> Cel7A and its E223S/ A224H/L225V/T226A/D262G mutant. <i>Biochemical Journal</i> , 2001, 356, 19.	3.7	29
60	Endoglucanase 28 (Cel12A), a new <i>Phanerochaete chrysosporium</i> cellulase. <i>FEBS Journal</i> , 1999, 259, 88-95.	0.2	75
61	Crystallographic evidence for substrate ring distortion and protein conformational changes during catalysis in cellobiohydrolase Cel16A from <i>Trichoderma reesei</i> . <i>Structure</i> , 1999, 7, 1035-1045.	3.3	164
62	High-resolution crystal structures reveal how a cellulose chain is bound in the 50 Å... long tunnel of cellobiohydrolase I from <i>Trichoderma reesei</i> 1 1Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1998, 275, 309-325.	4.2	413
63	The catalytic amino-acid residues in the active site of cellobiohydrolase 1 are involved in chiral recognition. <i>Journal of Biotechnology</i> , 1997, 57, 115-125.	3.8	25
64	The crystal structure of the catalytic core domain of endoglucanase I from <i>Trichoderma reesei</i> at 3.6 Å... resolution, and a comparison with related enzymes 1 1Edited by K.Nagai. <i>Journal of Molecular Biology</i> , 1997, 272, 383-397.	4.2	238
65	Isotherms for adsorption of cellobiohydrolase I and II from <i>Trichoderma reesei</i> on microcrystalline cellulose. <i>Applied Biochemistry and Biotechnology</i> , 1997, 66, 39-56.	2.9	65
66	Cellobiohydrolase I from <i>Trichoderma reesei</i> : Identification of an active-site nucleophile and additional information on sequence including the glycosylation pattern of the core protein. <i>Carbohydrate Research</i> , 1997, 304, 143-154.	2.3	63
67	Effect of potential binding site overlap to binding of cellulose to cellulose: a two-dimensional simulation. <i>FEBS Letters</i> , 1996, 378, 51-56.	2.8	22
68	The active sites of cellulases are involved in chiral recognition: a comparison of cellobiohydrolase 1 and endoglucanase 1. <i>FEBS Letters</i> , 1996, 390, 339-344.	2.8	54
69	Activity Studies and Crystal Structures of Catalytically Deficient Mutants of Cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Journal of Molecular Biology</i> , 1996, 264, 337-349.	4.2	162
70	Identification of functionally important amino acids in the cellulose-binding domain of <i>Trichoderma reesei</i> cellobiohydrolase I. <i>Protein Science</i> , 1995, 4, 1056-1064.	7.6	195
71	Cloning and characterization of a cDNA encoding a cellobiose dehydrogenase from the white rot fungus <i>Phanerochaete chrysosporium</i> . <i>FEBS Letters</i> , 1995, 369, 233-238.	2.8	61
72	Adsorption and synergism of cellobiohydrolase I and II of <i>Trichoderma reesei</i> during hydrolysis of microcrystalline cellulose. <i>Biotechnology and Bioengineering</i> , 1994, 44, 1064-1073.	3.3	97

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73	The three-dimensional crystal structure of the catalytic core of cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Science</i> , 1994, 265, 524-528.	12.6	605
74	A Combined Cellobiose Oxidase/Glucose Oxidase Biosensor for HPLC Determination On-Line of Glucose and Soluble Cellodextrines. <i>Analytical Biochemistry</i> , 1993, 214, 389-396.	2.4	39
75	Crystallization and Preliminary X-ray Studies on the Core Proteins of Cellobiohydrolase I and Endoglucanase I from <i>Trichoderma reesei</i> . <i>Journal of Molecular Biology</i> , 1993, 234, 905-907.	4.2	21
76	<i>Trichoderma reesei</i> has no true exo-cellulase: all intact and truncated cellulases produce new reducing end groups on cellulose. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1993, 1157, 107-113.	2.4	137
77	Analogues of the cellulose binding domain of cellobiohydrolase I from <i>Trichoderma reesei</i> : Synthesis and binding. , 1993, , 780-781.		0
78	A New Model For Enzymatic Hydrolysis of Cellulose Based on the Two-Domain Structure of Cellobiohydrolase I. <i>Nature Biotechnology</i> , 1991, 9, 286-290.	17.5	128
79	Isolated fungal cellulose terminal domains and a synthetic minimum analogue bind to cellulose. <i>FEBS Letters</i> , 1989, 243, 389-393.	2.8	76
80	A binding-site-deficient, catalytically active, core protein of endoglucanase III from the culture filtrate of <i>Trichoderma reesei</i> . <i>FEBS Journal</i> , 1988, 173, 179-183.	0.2	82
81	EGIII, a new endoglucanase from <i>Trichoderma reesei</i> : the characterization of both gene and enzyme. <i>Gene</i> , 1988, 63, 11-21.	2.2	313